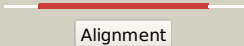
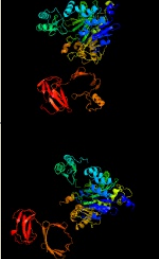
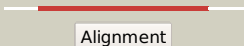
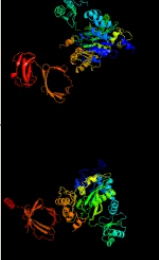
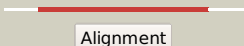
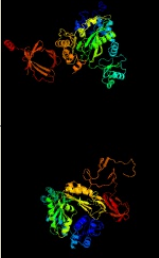





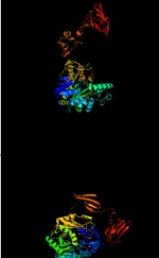
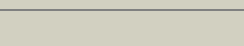
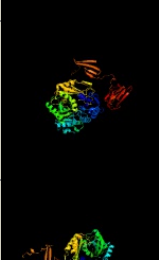



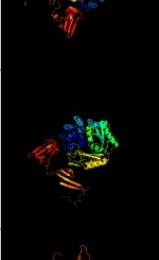
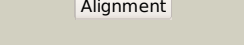














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3285_(accA3)_3666354_3668156
Date	Thu Aug 8 16:20:49 BST 2019
Unique Job ID	8dc30daa235fe6a6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5cslA_	 Alignment		100.0	30	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
2	c6g2dC_	 Alignment		100.0	31	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
3	c5cskB_	 Alignment		100.0	29	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
4	c3n6rK_	 Alignment		100.0	39	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
5	c3u9sA_	 Alignment		100.0	42	PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
6	c5vz0D_	 Alignment		100.0	43	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
7	c3hblA_	 Alignment		100.0	42	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
8	c4qskB_	 Alignment		100.0	43	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
9	c3bg5B_	 Alignment		100.0	43	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
10	c3tw6B_	 Alignment		100.0	46	PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
11	c4rcnA_	 Alignment		100.0	47	PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase

12	c2qf7A_	Alignment		100.0	44	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
13	c3va7A_	Alignment		100.0	45	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
14	c3bg5C_	Alignment		100.0	42	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
15	c4hmvB_	Alignment		100.0	44	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
16	c5i8iD_	Alignment		100.0	39	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
17	c4qslE_	Alignment		100.0	43	PDB header: ligase Chain: E: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
18	c4qslC_	Alignment		100.0	42	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
19	c3u9sE_	Alignment		100.0	43	PDB header: ligase Chain: E: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
20	c1w96B_	Alignment		100.0	31	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
21	c2hjwA_	Alignment	not modelled	100.0	32	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
22	c3u9sl_	Alignment	not modelled	100.0	46	PDB header: ligase Chain: I: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
23	c5mlkA_	Alignment	not modelled	100.0	100	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
24	c5ks8B_	Alignment	not modelled	100.0	46	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase subunit alpha; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
25	c5h80A_	Alignment	not modelled	100.0	41	PDB header: ligase Chain: A: PDB Molecule: carboxylase; PDBTitle: biotin carboxylase domain of single-chain bacterial carboxylase
26	c1ulzA_	Alignment	not modelled	100.0	44	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
27	c3ouzA_	Alignment	not modelled	100.0	40	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
28	c2vpqA_	Alignment	not modelled	100.0	45	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp

29	c5mlkB	Alignment	not modelled	100.0	96	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acc3 dimer from mycobacterium2 tuberculosis (rv3285)
30	c3g8cB	Alignment	not modelled	100.0	44	PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase in complex with biotin,2 bicarbonate, adp and mg ion
31	c2dzdB	Alignment	not modelled	100.0	44	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of pyruvate2 carboxylase
32	c2gpwC	Alignment	not modelled	100.0	44	PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
33	c3jzfA	Alignment	not modelled	100.0	47	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
34	c3gidB	Alignment	not modelled	100.0	31	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa carboxylase 22 (acc2) in complex with soraphen a
35	c1m6vE	Alignment	not modelled	100.0	19	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
36	c1kjaA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
37	c2xd4A	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
38	c2yyaB	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
39	c3uvzB	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
40	c3lp8A	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
41	c4dimA	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of phosphoribosylglycinamide synthetase from2 anaerococcus prevotii
42	c2ip4A	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
43	c3q2oB	Alignment	not modelled	100.0	20	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
44	c2qk4A	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase
45	c2dwcB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
46	c3orgA	Alignment	not modelled	100.0	18	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
47	c2ys6A	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
48	c3k5iB	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide
49	c4mamB	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: the crystal structure of phosphoribosylaminoimidazole carboxylase2 atpase subunit of francisella tularensis subsp. tularensis schu s4 in3 complex with an adp analog, amp-cp
50	c1gsoA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
51	c3votB	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase, bl00235; PDBTitle: crystal structure of l-amino acid ligase from bacillus

						licheniformis
52	c1vkzA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from <i>thermotoga maritima</i> at 2.30 a resolution
53	c3ax6C	Alignment	not modelled	100.0	19	PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from <i>thermotoga maritima</i>
54	c4ffnA	Alignment	not modelled	100.0	17	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
55	c4wd3B	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: l-amino acid ligase; PDBTitle: crystal structure of an l-amino acid ligase riza
56	d1w96a3	Alignment	not modelled	100.0	35	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
57	c5douC	Alignment	not modelled	100.0	19	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
58	c3etjB	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
59	c3vmmA	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: alanine-anticapsin ligase bacd; PDBTitle: crystal structure of bacd, an l-amino acid dipeptide ligase from <i>2 bacillus subtilis</i>
60	c3aw8A	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from <i>thermus thermophilus hb8</i>
61	c5vevB	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from <i>neisseria2 gonorrhoeae</i>
62	c3wvqA	Alignment	not modelled	100.0	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: pgm1; PDBTitle: structure of atp grasp protein
63	c2z04A	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from <i>aquifex aeolicus</i>
64	d1a9xa5	Alignment	not modelled	100.0	19	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
65	c5dotA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
66	c4fu0B	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase 7; PDBTitle: crystal structure of vang d-ala:d-ser ligase from <i>enterococcus2 faecalis</i>
67	c1ehiB	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdl2) of vancomycin-resistant2 <i>leuconostoc mesenteroides</i>
68	c3i12A	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: the crystal structure of the d-alanyl-alanine synthetase a from <i>2 salmonella enterica subsp. enterica serovar typhimurium str. lt2</i>
69	c2i80B	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: allosteric inhibition of <i>staphylococcus aureus</i> d-alanine:d-alanine2 ligase revealed by crystallographic studies
70	c3lwbA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from <i>2 mycobacterium tuberculosis</i>
71	c2r85B	Alignment	not modelled	100.0	15	PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from <i>pyrococcus furiosus</i> complexed with amp
72	d1ulza3	Alignment	not modelled	100.0	45	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
73	c6dgiA	Alignment	not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: the crystal structure of d-alanyl-alanine synthetase a from <i>vibrio2 cholerae o1 biovar eltor str. n16961</i>
74	c2dlnA	Alignment	not modelled	100.0	18	PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution
75	c2pn1A	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: carbamoylphosphate synthase large subunit; PDBTitle: crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from <i>exiguobacterium</i>

					sp. 255-15 at 2.00 a3 resolution
76	c3e5nA_	Alignment	not modelled	100.0	19 PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
77	c4egqD_	Alignment	not modelled	100.0	22 PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
78	c1e4eB_	Alignment	not modelled	100.0	20 PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
79	d2j9ga3	Alignment	not modelled	100.0	45 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
80	c2zdgA_	Alignment	not modelled	100.0	19 PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8
81	d2j9ga2	Alignment	not modelled	100.0	49 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
82	d1ulza2	Alignment	not modelled	100.0	52 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
83	d1w96a2	Alignment	not modelled	100.0	34 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
84	d1ulza1	Alignment	not modelled	100.0	30 Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
85	d2j9ga1	Alignment	not modelled	100.0	37 Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
86	c3tqtB_	Alignment	not modelled	100.0	17 PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
87	c3k3pA_	Alignment	not modelled	100.0	15 PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
88	c3se7A_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
89	c2pvpB_	Alignment	not modelled	100.0	12 PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
90	d1a9xa6	Alignment	not modelled	100.0	18 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
91	c3r23B_	Alignment	not modelled	100.0	15 PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
92	c5dmxC_	Alignment	not modelled	100.0	23 PDB header: ligase Chain: C: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
93	c4egjD_	Alignment	not modelled	100.0	25 PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
94	d1w96a1	Alignment	not modelled	100.0	21 Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
95	c5i47A_	Alignment	not modelled	100.0	20 PDB header: biosynthetic protein Chain: A: PDB Molecule: rimk domain protein atp-grasp; PDBTitle: crystal structure of rimk domain protein atp-grasp from sphaerobacter2 thermophilus dsm 20745
96	d1kjqA3	Alignment	not modelled	100.0	16 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
97	c4iwyA_	Alignment	not modelled	100.0	18 PDB header: ligase Chain: A: PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure
98	d1vkza3	Alignment	not modelled	100.0	17 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
99	d3etja3	Alignment	not modelled	100.0	20 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
100	c5ig8A_	Alignment	not modelled	100.0	12 PDB header: ligase Chain: A: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocylase mdnb from microcystis aeruginosa mrc
101	c3df7A_	Alignment	not modelled	100.0	13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative atp-grasp superfamily protein; PDBTitle: crystal structure of a putative atp-grasp superfamily protein from2 archaeoglobus fulgidus
102	c3vnhC_	Alignment	not modelled	100.0	13 PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase;

102	c3vpbc	Alignment	not modelled	100.0	13	PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate PDB header: biosynthetic protein
103	c1uc8B	Alignment	not modelled	100.0	18	Chain: B: PDB Molecule: lysine biosynthesis enzyme; PDBTitle: crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
104	c5ig9H	Alignment	not modelled	100.0	14	PDB header: ligase Chain: H: PDB Molecule: atp grasp ligase; PDBTitle: crystal structure of macrocyclase mdnc bound with precursor peptide2 mdna from microcystis aeruginosa mrc
105	d1w96c1	Alignment	not modelled	100.0	22	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
106	c5k2mG	Alignment	not modelled	99.9	14	PDB header: biosynthetic protein Chain: G: PDB Molecule: rimk-related lysine biosynthesis protein; PDBTitle: bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa
107	d1ehia2	Alignment	not modelled	99.9	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
108	d2r85a2	Alignment	not modelled	99.9	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
109	d1gsoa3	Alignment	not modelled	99.9	19	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
110	d2r7ka2	Alignment	not modelled	99.9	11	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
111	d1iowa2	Alignment	not modelled	99.9	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
112	c1i7nA	Alignment	not modelled	99.9	15	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
113	c1pk8D	Alignment	not modelled	99.9	14	PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
114	d1e4ea2	Alignment	not modelled	99.9	22	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
115	c2p0aA	Alignment	not modelled	99.9	15	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
116	c5csaA	Alignment	not modelled	99.9	20	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
117	c5ks8D	Alignment	not modelled	99.9	30	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
118	d1a9xa4	Alignment	not modelled	99.9	24	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
119	d1uc8a2	Alignment	not modelled	99.9	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain
120	c5ks8F	Alignment	not modelled	99.9	32	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus